

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 9, 2001, 09:08:03 ; Search time 997.13 Seconds
(without alignments)
15746.382 Million cell updates/sec

Title: US-09-001-737-7
Perfect score: 1661

Sequence: 1 GAATTCGGCTCATATGCA.....TGGCGGATAGCCGAATTC 1661

Scoring table: IDENTIFY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 1022815 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	261.8	15.8	878	146	BF275584	BF275584 GA_EB0002
2	257.2	15.5	1035	105	AL518632	AL518632 AL518632
3	254	15.3	977	152	BG321293	BG321293 Zm04.0450
4	253.4	15.3	988	106	AL532233	AL532233 AL532233
5	251.6	15.1	955	105	AL515262	AL515262 AL515262
6	249.6	15.0	811	151	BF627437	BF627437 HvMEB000
7	249.6	15.0	1017	105	AL515579	AL515579 AL515579
8	248	14.9	959	106	AL557150	AL557150 AL557150
9	246.4	14.8	980	106	AL557181	AL557181 EST300862
10	243	14.6	645	113	AM224051	AM224051 EST300862
11	239.4	14.4	716	156	D46006	D46006 R1C510372A
12	237.6	14.3	637	113	AM223768	AM223768 EST300579
13	236.2	14.2	668	115	AM329840	AM329840 EST298251
14	233	14.0	772	151	BF617440	BF617440 HvMEB001
15	227.4	13.7	680	114	AM330455	AM330455 HvMEB001
16	227.2	13.7	632	174	BG128308	BG128308 EST473954
17	226	13.6	790	155	BG599254	BG599254 EST504154
18	226	13.6	1351	167	BE422296	BE422296 HvMEB000
19	225.2	13.6	709	21	AL486676	AL486676 EST44998
20	222.2	13.4	825	138	BE642158	BE642158 C12.5.F2
21	222.2	13.4	660	152	BG354884	BG354884 HvMEB001
22	221.4	13.3	899	106	AL559862	AL559862 AL559862
23	220.8	13.3	930	106	AL559862	AL559862 EST265437
24	220.4	13.3	558	103	AL589594	AL589594 EST473908
25	219	13.2	710	174	BG128262	BG128262 EST473908
26	215.2	13.0	902	106	AL531904	AL531904 AL531904
27	214.4	12.9	817	152	BG344483	BG344483 HvMEB000
28	214.4	12.9	902	106	AL555787	AL555787 AL555787
29	214.2	12.9	870	152	BG344720	BG344720 HvMEB001
30	214	12.9	890	105	AL514684	AL514684 AL514684
31	212	12.8	787	155	BG594484	BG594484 EST498162
32	211.2	12.7	671	166	BE318972	BE318972 NF043012L
33	211	12.7	879	106	AL560505	AL560505 AL560505
34	210.8	12.6	710	163	BE131653	BE131653 L48-1652T
35	209.4	12.6	629	149	BF473185	BF473185 HvMEB000
36	208.8	12.6	715	155	BG592035	BG592035 EST295531
37	208.8	12.6	715	155	BG592035	BG592035 EST498877
38	208.4	12.5	955	105	AL517839	AL517839 EST470110
39	208.2	12.5	796	174	BG124548	BG124548 EST313366
40	207.4	12.5	739	118	AM622566	AM622566 EST313366
41	204.4	12.3	842	107	AU128717	AU128717 AU128717
42	204.2	12.3	926	106	AL536393	AL536393 AL536393
43	203.6	12.3	855	106	AL557977	AL557977 AL557977
44	202.2	12.2	857	106	AL532194	AL532194 AL532194
45	201.8	12.1	637	155	BG600875	BG600875 EST505770

ALIGNMENTS

RESULT 1
LOCUS BF275584 878 bp mRNA EST 07-MAR-2001
DEFINITION GA_EB00024G23f Gossypium arboreum 7-10 dpa fiber library Gossypium
arborescens cDNA clone GA_EB00024G23f, mRNA sequence.
ACCESSION BF275584
VERSION BF275584.1 GI:11206654
KEYWORDS EST
SOURCE Gossypium arboreum.
ORGANISM Gossypium arboreum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE 1 (bases 1 to 878)
AUTHORS Wing, R.A., Fritsch, D., Yu, Y., Mait, D., Rambo, T., Simmons, J., Henry
D., Wood, T.C., Leslie, A., and Wilkins, T.A.
TITLE An integrated analysis of the genetics, development, and evolution

JOURNAL COMMENT

of the cotton fiber
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACACTCAGTAAAGG
High quality sequence stop: 716.
Location/Qualifiers
1. 878
/organism="Gossypium arboreum"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone_lib="GA_EB0024G23f"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/note="Vector: pBR-CMV; Site_1: EcoRI; Site_2: XhoI"

FEATURES

BASE COUNT 253 a 157 c 219 g 245 t 4 others
ORIGIN
Query Match 15.8%; Score 261.8; DB 146; Length 878;
Best local similarity 58.1%; Pred. No. 1.4e-62;
Matches 458; Conservative 0; Mismatches 330; Indels 0; Gaps 0;
481 TTGAGAGATATATCTGAGAGATATGACCGTGGCAACGATGATGATTAACATCG 540
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28 TTGAGAGATATATCTGAGAGATATGACCGTGGCAACGATGATGATTAACATCG 87
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
541 AAGATTCGAGGATGAGAAAGAGATGAGATGAGATGAGATGAGATGAGATGAG 600
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
88 ACTCATCT 147
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601 GTTACCTGTCATATCATGATGATGATGATGATGATGATGATGATGATGATGATG 660
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148 GTTACCTGTCATATCATGATGATGATGATGATGATGATGATGATGATGATGATG 207
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661 CATTTATTTATTCAGAGATGATGATGATGATGATGATGATGATGATGATGATG 720
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781 CACTTCCACCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 840
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901 GTTACAGATTTACAGAGATGATGATGATGATGATGATGATGATGATGATGATG 960
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448 CTGATTCAGACTAGTATGATGATGATGATGATGATGATGATGATGATGATG 507
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1081 CTGACTTGTACCTGAAAACTGAAAGATGATGATGATGATGATGATGATGATG 1140
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Db 628 CTCTGTAATTCAGAAAAATTTGGCAGAAAGATTCCTCAAACTATCTGCTGTTGTCAG 687

QY 1141 TTATCAACTAGAGCTCCACAGACAGACCTTTAAAGAAATGAACTTGCATGAG 1200

Db 688 TCATTAAGCTGGGCTCCACAGACAGACCTTTGAGATGCTGACGATTTGAG 747

QY 1201 ATGCTTAATGCTACAGCTGACGCTTGAAGAGATTCGTTGCTGCTGTTGAGAAC 1260

Db 748 ATGCAAGAAATGCTACATTTGCTGCTCATAGNAGATTTGCTGCTGCTGCTGCTG 807

QY 1261 CACTATT 1268

Db 808 CCTTAGT 815

RESULT 2

AL518632 1035 bp mRNA EST 13-FEB-2001

LOCUS AL518632 LTI_NFL011_NBC1 Homo sapiens cDNA clone CSODN009Y115 5

DEFINITION prime, mRNA sequence.

ACCESSION AL518632

VERSION AL518632.1 GI:12782125

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex France

Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

Source

Location/Qualifiers

1..1035

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CSODN009Y115"

/clone_1b="LTI_NFL011_NBC1"

/sex="male"

/tissue.type="neuroblastoma cells"

/lab_host="DH10B"

/note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 311 a 195 c 259 g 266 t 4 others

ORIGIN

Query Match 15.58; Score 257.2; DB 105; Length 1035;

Best Local Similarity 56.38; Pred. No. 2.9e-61;

Matches 500; Conservative 1; Mismatches 384; Indels 3; Gaps 1;

QY 18 GCAAAAGAAATCAATTTTTCAGAGATGCGCGTGCATGCTGCGCGGAGCTTGAATG 77

Db 116 GCCAAAGATGTAATTTTGGTCAGATGCCCGAGCTTAATGCTTCAAGAGTGAACCTT 175

QY 78 TTAGCAGATACCGTCAAGTAAGCTGTGCTCAAGGCGCGAATGTTGTTTGAAGAA 137

Db 176 TTAGCCGATGCTGTGCGCTTACCAATGGGCGCAAGGGAACGATGATTATTGAGCAG 235

QY 138 GCTTTGTTCCCTTAATTAATGACGGGGTAAACCATGCTTAAGAGATCAATTA 197

Db 236 AGTTGGGAGAGTCCCAAGTAACAAAAGATGTTGACTGTTGCCAAGTCAATTGACTTA 295

QY 198 GAAGATCATTTTGAAGAAATGAGAGCAAAATGTTGCTGCAAGAGCTTCAAAACCAT 257

Db 296 AAAGATTAATACAAAACATGAGCTAACTTTGTAAGATGTGTCCATATACACAAAT 355

QY 258 GATATGCTGTTGGGAGAGCTACTGCAACAGTTTGGACACAGCATTTGCTATGAA 317

Db 356 GAAAGAGCTGGGATGAGCTACACAGCTGCTACTGCTGAGCGCTCTTAAGCAGAGAA 415

QY 318 GCACTAAAAATGTGACAGCAGCTCTAATCCATTGGTATCCGTGAGGAGCATTTGAACA 377

Db 416 GCTTCGAGAAATAGCAAAAGTCTAATCCAGTGAATATGAGAAAGAGTGTGATGTTA 475

QY 378 GCAACAGCAACAGCTGTGAGACCTTGAAGCCATTCCTCAACCTGTATCTGCAAGAA 437

Db 476 GCTGTTATGCTTATTTCTGATCACTTAAAGACGCTTAACCTGTGACACCCCTTAA 535

QY 438 GCTATTGCTGAGTCCCTGCAATATCATCAGCTCTGAAAAAG--TTGAGAGATATATC 494

Db 536 GAAATTCACAGAGTTGCTACGATTTCTGCAAAACGAGACAAAGAAATGCGAATATCATC 595

QY 495 TCAGAGCTATGAGCGCTGTGGGCAAGATGTTGATTCATCGAAGAAATCTGAGCT 554

Db 596 TCTGATGCAATGAAAAAGTTGAGAAAGAGGTCTATCAGATTAAGATGAAAAACA 655

QY 555 ATGAAAACAGAACTTGAAGCTTGAAGGCAATTTGACCGTGTACCTGCTCA 614

Db 656 CTGAAGATGAAATTTGAATTAATTAAGGCAATSCCGTTGATGAGGCTATATTCTCA 715

QY 615 TACATGATCAGACAAATGAAAAATGTTGCAACCTTGAAGCCATTTATCTATATC 674

Db 716 TACTTATTAATATCATCAAAAGGTGAGAAATGGAATTCAGAGTCCATGTTCTGTG 775

QY 675 ACGATTAATAAGTGTCAACATCCAGACATTTGCGACTTGTGAGAGTTCTTAA 734

Db 776 AGTGAATAAATAATTTCTATGATTCAGCTCAATGCTGCTGTTGAATGCCAATGCT 835

QY 735 ACCAACCGTCAATCATATTATTCAGATGATGATGATGATGATGATGATGATGATGAT 794

Db 836 CACCGTACCTTTGCTATATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 895

QY 795 GTCTGACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 854

Db 896 GTCTTAAATAGCTTAAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 955

QY 855 GATGCTGCTGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 902

Db 956 TGACATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1003

RESULT 3

BG321293

LOCUS BG321293 977 bp mRNA EST 27-FEB-2001

DEFINITION Zm04_04909_R Zm04_04909_AATC_ECORC_cold_stressed_maize_seedlings Zea mays

ACCESSION BG321293

VERSION BG321293.1 GI:13150971

KEYWORDS EST.

SOURCE Zea mays.

ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

AUTHORS Singh, J.A., Wakui, K., Couroux, P., De Moor, A., Harris, L.J., Hattori, J.I., Ouellet, T., Robert, L.S., Spolt, D. and Rinker, N.A.

TITLE Expressed Sequence Tags from Cold-Stressed Maize Seedlings

JOURNAL Unpublished (2001)

COMMENT Contact: Singh, J.A.

Eastern Cereal and Oilseed Research Centre

Agriculture and Agri-Food Canada

960 Carling Avenue, Bldg. 20, Ottawa, Ontario, K1A 0C6, Canada


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Db 415 GCGTCGAGAAAGATTAGCAAGGTGTAATCCAGTGAATAGAGAGGTGTATGTTA 474
Oy 378 GCAACAGCAAGAGCTGTGAGAGCCTTGAAGACCTATGCTCAACCTGTATCTGGACAGAA 437
Db 475 GCTGTGATGCTGTATATGCTGAATCTTAAAGACACTTAAACCTGTGACACCCCTG 534
Oy 438 GCTATGCTCAGGTGCTGCAATATCATCAGCTGTGAAAAG--TTGAGAGTATATC 494
Db 535 GAAATTCACAGGTGCTGATGATTTCTGCAAGGAGCAAGAAATTTGCAATATCATC 594
Oy 495 TCAGAGCTATGAGCGGTGGGCAAGATGCTGATTTACATCGAAGATCTCAGGT 554
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Oy 555 ATGGAACAGAACTTGAAGTGTGAAGGATGCAATTTGACCGTGTACTGTCTCAA 614
Db 655 CTGAATGATGATTAAGAAATTAATGAAGCATGAAAGTTGATGACAGCTATTTCTGCA 714
Oy 615 TACATGCTCAGACATGAAAAAATGTTGACACCTTGAAGACCTTATCTTAATC 674
Db 715 TACTTATTAATACATCAAAAGTCAAAATGTGAATTCAGATGCTATGTTCTGTG 774
Oy 675 ACGGATAAAAAGTGTCAAAACATCAAGCATTTTGGCAGTACTTGAAGAGTCTTAA 734
Db 775 AGTGAAGAAAAATTTCTAGTATCAGTCCATTTGACCTGCTTGAATTTGCCAATGCT 834
Oy 735 ACCAAGCTCCATCTACTATTATTCAGATGATGATGATGATGATGATGATGATGATG 794
Db 835 CACCGTAAGCCTTTGGTCAATATCGCTGAAGATGTGATGATGATGATGATGATGATG 894
Oy 795 GCTTGAAACAGATTTCTGTACTTCAATGCTGTGCTGCTGAAGCCAGAGATTTGCT 854
Db 895 GCTTGAAATGAGCTTAAAGTTGCTTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 954
Oy 855 GATCGTCTGAAGCTATGCTTGAAGACATTTGCTAT 889
Db 955 GACAATAG-AAAGACAGCTTAAAGATATGCTAT 988

RESULT 5
AL15262 955 bp mRNA EST 13-FEB-2001
LOCUS AL15262 L1-NFL006_PL2 Homo sapiens cDNA clone C10B0162A04 5
DEFINITION AL15262 L1-NFL006_PL2 Homo sapiens cDNA clone C10B0162A04 5
ACCESSION AL15262
VERSION AL15262.1 GI:12778755
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 955)
AUTHORS L.I.W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
Source
Location/Qualifiers
1..955
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="C10B0162A04"
/location="L1-NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,"

```

```

Query Match 15.18; Score 251.6; DB 105; Length 955;
Best Local Similarity 57.08; Pred. 1.1e-59;
Matches 480; Conservative 0; Mismatches 359; Indels 3; Gaps 1;

BASE COUNT 288 a 181 c 236 g 247 t 3 others
ORIGIN
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@life.com URL :
http://fulllength.invitrogen.com"

18 GCAAGAAATCAAAATTTTCAGACATGCGCTGCAATGCGCGAGTGTATG 77
Db 114 GCCAAGATGTAAATTTGGTGCATATCCGACCTTATGCTTAAGGTATACCTT 173
Oy 78 TTACAGATATCCCTCAAAATGACCTTGTGCTTAAAGGCGCATGTTGTTGAAA 137
Db 174 TTACGCGATGCTGCGCTTCAATGAGGCGCAAGGAAAGACGTGATTTATGACG 233
Oy 138 GCTTTGTTCTCCCTTAATTAATGACGGGTAAACATGCTTAAAGATGCAATTA 197
Db 234 AGTGGGGAGTCCCAAGTACAAAGATGATGCTGCTTCAAGATCATGACTTA 293
Oy 198 GAAGATATTTGAAGAAATGAGGACCAAAATTTGCTGCTGAAGTCTTAAACCAAT 257
Db 294 AAGATTAATACAAAACATTTGAGACTTAACTTTCAATATTTCCATACCAAT 353
Oy 258 GATATTGCTGTGATGAGGACGACTACGCAAGATTTTGAACAGACCAATTTGCTG 317
Db 354 GAGAGAGCTGGGATGCGCACTACCACTCTCTACTGTCGACGCTCTATCCAAAG 413
Oy 318 GGAATAAAAAATGTGACAGCAGGTGCTATGCAATTTGCTGCTGCTGCTGCTGCT 377
Db 414 GCGTGGAGAGATTAAGCAAGGTGCTATATCAATGCAATGCAATGCAATGCAATG 473
Oy 378 GCAACAGCAAGAGCTGTGAAAGCTTGAAGCCATTTGCTCACTGCTGCTGCTG 437
Db 474 GCTGTGATGCTGTATGCTGCACTTAAAGAGTTTAACTGTTACCACTGCTGCT 533
Oy 438 GCTATGCTCAGGTGCTGCAATATCAATGCTGCTGCTGCTGCTGCTGCTGCTG 494
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Db 594 TCTGATGCAATGAAAAAGTTGGAAGAGGCTGCTGCTGCTGCTGCTGCTGCTG 653
Oy 555 ATGGAACAGAACTTGAAGTGTGAAGGCTCAATTTGACCGTGTATCTGCTCAA 614
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Oy 795 GCTTGAAACAGATTTCTGTACTTCAATGCTGTGCTGCTGCTGCTGCTGCTGCT 854
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Db 954 GA 955

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[illegible]

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Oy	948	ATGACAGCCCTTGGAGAGGCTGCTAATAATTACAGTGTGAATTAAGAATAGACAGCTAATGTT	1007	
Db	361	AACACATCTTAGAAGACGGCTGCACAAGGTGTCTTCACAAAAGAACTGCACAAACATGTT	420	
Oy	1008	CAGAGTTCAGGAAGTTACAGAACGTAATGTCCTAACCGTATTCACATGATTAATTCGCAATTA	1067	
Db	421	GGTATGGCAGCACCCAGAGGAAGTACTACATMAAGGGTTGGCCACAGATCAAAAAATCTCAT	480	
Oy	1068	GAACAACAACCTCTGACTTTGACCCTGGAAAACTCACAAGAACGTTGGGGAAATTAAGCT	1127	
Db	481	GAGGTACACAGACAGACTACGACAGAAAGAAAATTCATGAGAGATTTGCAAAGCTCGCC	540	
Oy	1128	GGTGGTGGAGCTGTTATCAAAAGTGAGAGCTCCACACAGACAGCCTTTAAAAAGAAATGA	1187	
Db	541	GGTGGTGGAGCTGTTATCAAAAGTGAGAGCTCCACACAGACAGCCTTTAAAAAGAAATGA	600	
Oy	1188	CTTCGCATTGAGGATGCTCTAAATAGTCAACGACGACGCCGTTGGAAGAGTATGCTGCT	1247	
Db	601	TTCGGAGTTGAGAGATGCTCTAAACGCAACATATGCTGCCGTTGAGGAAGTATGTGTT	660	
Oy	1248	GGTGGTGGAAACGACCTATTATACGCTATTATGAAAAAGTACAGC	1291	
Db	661	GGTGGAGGCTGCACCTTTTATGAGCTGGCTGCTGAAGTTGATGC	704	
RESULT	7			
AL515579				
LOCUS	AL515579	1017 bp	mRNA	EST
DEFINITION	AL515579 LTI_NFL011.NBC1 Homo sapiens cDNA clone CSDBA002YD20	13-FEB-2001		
FEATURES	prime, mRNA sequence.			
ACCESSION	AL515579			
VERSION	AL515579.1 GI:12779072			
KEYWORDS	EST			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
REFERENCE	1. (bases 1 to 1017)			
AUTHORS	L.I.W.B., Gruber,C., Jesse,J. and Polayes,D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr. Location/Qualifiers			
FEATURES				
source				
	1..1017			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/clone="CSDBA002YD20"			
	/clone_1lb="LTI_NFL011.NBC1"			
	/sex="female"			
	/tissue.type="neuroblastoma cells"			
	/lab_host="DH10B"			
	/note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(ct) primer. Five prime end cloned, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com url : http://fulllength.invitrogen.com"			
BASE COUNT	308 a	191 c	235 g	261 t
ORIGIN				2 others
Query Match	15.0%	Score 249.6;	DB 105;	Length 1017;
Best Local Similarity	56.8%;	Pred. No. 4e-59;		

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	Li, W. B., Gruber, C., Jesse, J. and Polayes, D.	Full-length cDNA libraries and normalization	Unpublished (2001)	
2	Genoscope - Centre National de Sequencage	BP 191 91006 EVRY cedex - France	Email: sequef@genoscope.cns.fr , Web : www.genoscope.cns.fr .	
3	Location/Qualifiers	1. 959		
4	/organism="Homo sapiens"			
5	/db-xref="taxon:9606"			
6	/clone="CSDBH0021B12"			
7	/clone_11b="L1-FLO12.TC1"			
8	/tissue="type="T cells from T cell leukemia"			
9	/lab_host="DH10B"			
10	/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filiang@lifetech.com URL : http://filllength.invitrogen.com "			
11	BASE COUNT	291 a	183 c	238 g
12	ORIGIN	183 c	238 g	246 t
13	1 others			
14	Query Match	14.9%	Score 248;	DB 106;
15	Best Local Similarity	56.7%	Pred. No. 1,1e-58;	Length 959;
16	Matches 477; Conservative	1;	Mismatches 361;	Indels 3; Gaps 1;
17	18 GCAGAAAGATCAATATTTCAGCAGATGCGCGTGTGCATGTCGCCGAGTGTATG 77			
18	118 GCCAAAGATGTAAATTTGTGTGCAGATGCCCGAGCCTTAATCTTCAAGGTGTAGACCT 177			
19	78 TTAGCAGATACCGTCAAGATACGACTGTGGCTAAAGGGCCAGTATGTTCTTGAANA 137			
20	178 TTAGCCGATGCTGTGGCGCTTACATAGGGGCCAAGAGAACACATGATATTATGACAG 237			
21	138 GCTTTGGTTTCTCCCTTAATTACTATGACGGGGTAACCAATGCTTAAGAGATCGAATTA 197			
22	238 AGTTGGGGAAGTCCCAAGTAAACAAAGATGGTGTGACTGTTCGCAAGTCAATGTGACTTA 297			
23	198 GAAGTCATTTTGAACAATGGAGCAAAATGTGTCTGACAGAGGCTTTGAACCAAGCATTTGTA 257			
24	298 AAGATTAATTAACAAGAACATTTGGAGCTAACTTGTTCAGATGTGCCATTAACACAAAT 357			
25	258 GATATTCTGTATGGAGGAGCTACTCTGCACACAGTTTGGACACAGCAATGTTTCATGAA 317			
26	358 GAAGACCTGGGATGGACCTACCACTGTACTGTACTGACAGCTCTTAAGCCAAAGGAA 417			
27	318 GGCATTAATAATTTGACAGAGGCTCTAATCAATTGTATCCGTGAGGACATTTGAACA 377			
28	418 GGGCTTGAGAAAGTTTGAACAAAGTCTAATCACTGGAATACAGAGAGGTGTATGTTA 477			
29	378 GCAACAGCAACAGCTGTTGAACCTTGAACCCATTGCTCAACCTTACTGTGCAAGAA 437			
30	478 GCTGTGATGCTGATGCTGTAATGCTGAACCTTAAGACAGCTTATGTGACCAACCCCTTAA 537			
31	438 GCTATGCTCAGGTGGCTGCTGATCATCAAGCTCTGAAANAAG - -TTGAGAGATATATC 494			
32	538 GAATTTGCCACAGGTGCTACGATTTCTGCAAAAGGAGACAAAGAAATTTGGCAATATCATC 597			
33	495 TCAGAGCTATGAGACCTGTGGGCAAGAGTGTGTATTCATCGAAGAAATTCGAGCT 554			
34	598 TCGATGATCAATGAAAGAGTTGGAAGAAAGGTGTCTACAGTAAAGATGGAAGAAACA 657			
35	555 ATGGAAGCACTGAAGGTGTTGAAGGATGCAATTTGACCGGTGTTACTCTGTCAA 614			

TITLE / Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
JOURNAL Unpublished (1999)
COMMENT Contact: David Frisch
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrisch@clemson.edu

FEATURES
source Location/Qualifiers

1. 645
/organism="Lycopersicon esculentum"
/cultivar="7A496"
/db_xref="taxon:4081"
/clone="CLEN489"
/clone_1lb="tomato fruit red ripe, TAMU"
/tissue_type="pericarp"
/dev_stage="red ripe (7-20 days post-breaker)"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Supplier: Giovannoni. Fruit were tagged at the
breaker stage (first sign of lycopen accumulation on the
blossom end of the fruit) and harvested 7 days
post-breaker (fully red-ripe). 10 days post breaker, and
20 days post-breaker (over-ripe). 20 day fruit which
showed external or internal signs of pathogenesis were
discarded. Fruit were cut in half and the seeds and
locules were discarded prior to freezing the pericarp."

BASE COUNT 205 a 102 c 166 g 172 t
ORIGIN

Query Match 14.6%; Score 243; DB 113; Length 645;
Best Local Similarity 61.1%; Pred. No. 2,4e-57;
Matches 393; Conservative 0; Mismatches 250; Indels 0; Gaps 0;

QY 607 TGTCTCATACATGTCACACAGCAATGAAAAATGGTTCGACCTTGAACCCATTGA 666
DB 2 TGTCTCTCTACTTGTTCACGACGTGAGAAAAATGTCCTTGAATGTGAACTGTAGT 61
QY 667 TCTTATACAGGATAAAAAGTGCACATCCAGCATTTTGCACACTTGTGAGAG 726
DB 62 TGTCTACTGTTGATAAAAAGATACAAATGCAAGATCTTGTATATGTCCTGAAAGT 121
QY 727 TTTCTAAACCAACGCTCATCTACTTATGAGATGATGATGATGATGATGATGAT 786
DB 122 CTATCAGAAATGTTACCAATTTTAAATTTGCTGATGATGATGATGATGATGATG 181
QY 787 CAACCTTGTCTGACAGATTCGTGATCTTCAATGATGATGATGATGATGATGATG 846
DB 182 CAACCTTGTCTGACAGATTCGTGATCTTCAATGATGATGATGATGATGATGATG 241
QY 847 GATTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 906
DB 242 GTTTGGTATGAGGAAAAAGCAGATTCCTGATGATGATGATGATGATGATGATGAT 301
QY 907 TGAATACAGAGATCTAGAGCTTAAATTAAGATGCTCAATGATGATGATGATGATG 966
DB 302 TTAATGAGGAGAGCTTGGCTTACCTTGGACAGGCTGACAAAGAAATGCTAGATC 361
QY 967 CTGCTAAGATTACAGTTAAAGATGACAGATTAAGTGTGATGATGATGATGATGAT 1026
DB 362 CTGCTAAGATTACAGTTAAAGATGACAGATTAAGTGTGATGATGATGATGATGAT 421
QY 1027 AAGCTATTGCTAACCGTTTGCATGATTAATGCAATTAAGAAACAACACTTGTGAT 1086
DB 422 AAGCACTCAACAAAGGTTGACAGATTAAGAAACCTAATGAGCTGACATCAAGAT 481
QY 1087 TTGACCGTGAAGAACTACAGAGCTTGGCGAAATTTAGCTGATGATGATGATGATG 1146
DB 482 ATGAAAGGAAAGCTAAATGAAGATTTGATGATGATGATGATGATGATGATGATG 541

QY 1147 AAGTAGAGCTCCACAGACAGACCTTTAAAGAAATGAACCTGCGATGAGATGCTC 1206
DB 542 AGCTTGAGAGCTCAACAGTGAACAGTAATGAGAGAGAACTTAGAGTGAAGATGCTC 601
QY 1207 TAAATGCTACAGCTGACGCGCTTGAAGAGATGATGCTGCTGG 1249
DB 602 TCAATGCAACAAAGCAGCTGTTGAGAGAGATGATGCTGCTGG 644

RESULT 11
LOCUS D46006 716 bp mRNA EST 09-MAR-2000
DEFINITION R1CS10372A Rice green shoot Oryza sativa cDNA, mRNA sequence.
ACCESSION D46006
VERSION D46006.2 GI:7212768
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 716)
Sasaki, T., Miyao, A. and Yamamoto, K.
Rice cDNA from callus 1995
Unpublished (1995)
On Mar 9, 1995 this sequence version replaced gi:699715.
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
Ibaraki,
Japan 305
Tel: 0298-38-7441
Fax: 0298-38-7468
Email: tsasaki@abrr.affrc.go.jp
PROJECT "RGP"
Sequence updated (01-Mar-2000).

FEATURES
source Location/Qualifiers

1. 716
/organism="Oryza sativa"
/strain="Nipponbare"
/db_xref="taxon:4530"
/clone_1lb="Rice green shoot"
/note="Green shoot (8 days old)"
BASE COUNT 222 a 120 c 198 g 175 t 1 others
ORIGIN

Query Match 14.4%; Score 239.4; DB 156; Length 716;
Best Local Similarity 58.6%; Pred. No. 2,6e-56;
Matches 414; Conservative 0; Mismatches 292; Indels 0; Gaps 0;

QY 550 GAGGATATGAAAGCACTGGAAGTGTGAGAGCATGCAATTTGACCGTGTACCTGT 609
DB 5 GAAATTCGAGAAATATCTATATGTTGTGAGAGATGCACTTGAACGGTGTATATCT 64
QY 610 CTCAATACATGCTACACAGATGAAAAAATGTTGACAGACTTGAACCACTTATCT 669
DB 65 CCCGATATTTGTAACGACAGGCAAGAAATGTCGAGAAATGATGAGAACTGCAACTTC 124
QY 670 TATACGAGTAAAGAAAGTGTCAACATCCAGACATTTTCCACTTGTGAGAGATG 729
DB 125 TTTTGGTGAACAAAAAATGACCAAGGAGATCTTATCAATGTTTGGAGAGGCA 184
QY 730 TTAAGAACACGCTTATCTATATTTGACAGATGATGATGATGATGATGATGATG 789
DB 185 TTAAGAGTCAATCCCAATTTGATAATTTGCTGAGAGATTTGAGAGGAGGCTTGTCTA 244
QY 790 CCTTGTCTTGAACAGATTCGTGATCTTCAATGATGATGATGATGATGATGATGAT 849
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QY 850 TTGATGATGCTGTAAGCTATGCTTGAAGACATTTGATCTTGAAGAGTGTGATGATG 909

Db 305 TTGGTAGCCCAAGACCCTACTGATGATATTCATTCATTCAGACCACTGTA 364
 Oy 910 TTACAGAGATCTAGACATTTGAATTTAAAGATGCTACATGACAGCCCTTGACAGGCTG 969
 Db 365 TCAGGGATGAAAGTGGGCTGCTACCTTGACAAAGCAGCAATATGTTTGAAGACGCTG 424
 Oy 970 CTAAAGATTACAGTGTATTAAGATACAGATTAATTTGTAAGTTGAGAGATTCAGAG 1029
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 Oy 3030 CTATGCTAACCTGATGATGATTAATTCGCAATAGAAACACACTTGTGACTTTG 1089
 Db 485 AAGTGTACAGAGGCTGACAAATAAATAATCAACGAGCTGCCGAACAAGATACG 544
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 Db 665 ATGCTACAGAGCTGCTGCTGAGAGAGATATGTTGCTGCTGCTGCTGCTGCTG 710

RESULT 12

AM233768 637 bp mRNA EST 07-DEC-1999
 LOCUS EST300579 tomato fruit red ripe, TAMU Lycopersicon esculentum cDNA
 DEFINITION clone cLENI3H9, mRNA sequence.
 ACCESSION AM233768
 VERSION AM233768.1 GI:6535452
 KEYWORDS EST.
 SOURCE tomato.
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
 Lycopersicon.
 1 (bases 1 to 637)
 Alcala, J., Vrebalov, J., White, R., Matern, A.L., Holt, I.E., Liang, F.,
 Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Romning, C.M.,
 Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
 Generation of ESTs from tomato fruit tissue
 Unpublished (1999)
 Contact: David Frisch
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 4366
 Fax: 864 656 4293
 Email: dfrisch@clemson.edu

FEATURES

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 5 prime sequence.
 Location/Qualifiers
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 /db_xref="taxon:4081"
 /clone="cLENI3H9"
 /clone_1b="tomato fruit red ripe, TAMU"
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 /dev_stage="red ripe (7-20 days post-breaker)"
 /note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2:
 XhoI; supplier: Giovannoni; Fruit were tagged at the
 breaker stage (first sign of lycopen accumulation on the
 blossom end of the fruit) and harvested 7 days
 post-breaker (fully red-ripe) and harvested 20 days
 post-breaker (over-ripe). 20 day fruit which
 showed external or internal signs of pathogenesis were
 discarded. Fruit were cut in half and the seeds and

BASE COUNT 204 a 102 c 163 g 168 t
 locules were discarded prior to freezing the pericarp.
 ORIGIN

Query Match 14.3%; Score 237.6; DB 113; Length 637;
 Best Local Similarity 60.8%; Pred. No. 8, 1e-56;
 Matches 387; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

Oy 607 TGTCTCAATACATGCTGACAGACATGAAAAAATGCTTGACAGACCTTGAAAAACCATTTA 666
 Db 2 TCTCTCTTACTTGTGTACCGACAGTAGAAAAATGTCCTGTGAATATGATGAGATGACT 61
 Oy 667 TCTTAATACAGATTAATAAAGTGTCAACATCCAAACATTTTGGCTACTTACTGAGAG 726
 Db 62 TGCTAGCTGTATATAAAGATTAACAATGCAAGAGATCTTGTATATCCTGAGAGATG 121
 Oy 727 TTCTTAACCAACCGCTCATTACTCTATTTCAGATGATGATGATGATGATGATGATG 786
 Db 122 CTATCAGAAATGTTACCAATTTTAAATTTCTGAAAGATTAATGACGAGACCTTTG 181
 Oy 787 CAACCTTCTTGAACAGATGCTGCTACTTCAATGCTGCTGCTGCTGCTGCTGCTGCTG 846
 Db 182 CAACCTTCTGCTCAATAGCTTAGAGTGCCTTGAAGTGCCTGCTCACTTAACTCTG 241
 Oy 847 GATTGATGATGCTGTAAGCTATGCTTGAACATGCTATCTTGAACAGCTGTAACAG 906
 Db 242 GTTTGTAGGCAAAAAGCCATGATGATGATGATGATGATGATGATGATGATGATGATG 301
 Oy 907 TGATTACAGAGATCTAGAGCTTGAATTAAGATCTCAATGACAGCCCTTGAGAGAG 966
 Db 302 TTATTAGGAGAGAGCTTGCTTACCTTCTTGAACAGCTGACAGAGATCTTAGTCAATG 361
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 Db 362 CTCTTAAGATGATGCTGCTGATGAGATGCTGCTGATGATGATGATGATGATGATG 421
 Oy 1027 AAGCTATTCTTAACCGATTGCTGCTGATTAATTCGCAATTTGAACCAACATCTTGACT 1086
 Db 422 AACCACTCAACAAAGCTGCTGACATTAATAAAGCTGATGAGCTGACAGATCAAGATT 481
 Oy 1087 TTGACCGTGAATAACTACAAAGAGCTTGGCGAAATTAAGCTGCTGCTGCTGCTGCTG 1146
 Db 482 ATTAAGAGAAAGATTAATTAAGATTAATGATTAATGATTAATGATTAATGATTAATG 541
 Oy 1147 AAGTAGAGCTTCAACAGAGACCTTTAAAGAAATGAACCTGCAATTTGAGAGATGCT 1206
 Db 542 AGGTTGAGCTCAAACTGAATGTAAGAGAGAGAACTTGAAGTAGAGATGATGCTGCT 601
 Oy 1207 TAAATGCTACAGCTGACGCTTGAAGAGATGCTG 1242
 Db 602 TCAATCAACAAAGCAGCTTTGAGAGAGATTTTG 637

RESULT 13

AM398404 668 bp mRNA EST 07-FEB-2000
 LOCUS EST298251 L. pennellii trichome, Cornell University Lycopersicon
 DEFINITION pennellii cDNA clone clPT6M1.5' similar to similar to nearly
 identical to Solanum tuberosum chaperonin-60 beta subunit, mRNA
 sequence.

ACCESSION AM398404
 VERSION AM398404.1 GI:6916874

KEYWORDS EST.
 SOURCE Lycopersicon pennellii.

ORGANISM Lycopersicon pennellii.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum;

Lycopersicon.
 1 (bases 1 to 668)

Alcala, J., Vrebalov, J., White, R., Matern, A.L., Lakey, J., Holt, I.E.,
 Liang, F., Hansen, T.S., Upton, J., Romning, C.M., Craven, M.B., Fujii

Oy 658 ACCATTATATCATACAGGATTAAGTTCACATCAAGCATTTTCCACTAC 717
 Db 217 ACATGACAGCTGCTTTGGTTGGTACAGAAATCACCAAGCAGGAGCTTATCAATGTTG 276
 Oy 718 TTGAGGAAGTCTTAAACCAACCGTCCATTAATCTATTTGAGATGATGATGTTG 777
 Db 277 TGGAGAGGCAATTTAGGGGTCAATACCAATCCGATCTGAGATTTGAGACAG 336
 Oy 778 AGGACTTCCAAACCTTGTCTTGAACAAGATTGCTGATTTCAATGCTGCTGCTCA 837
 Db -337 AGGCTTTCACACCTTGTGTGCAACCAAGCTAAGAGTTTGTGAAATCTGTGCTATCA 396
 Oy 838 AAGGCCAGAGATTTGGTGTATGCTGTAAAGCTATGCTTGAAGCATTTGCTATCTTGACAG 897
 Db 397 AAGCCCTGCTTTTGGAGAGCGCAAGACCCAGTACCTGGACGACATTTGCCCTCCACCG 456
 Oy 898 GTGTACAGTATGATACAGAGATCTAGAGCTTGAATTAAAGATGCTAATGACAGGCC 957
 Db 457 GAGGAACCTGTATACAGACAGAGGTTGACTCACACTTGACAAAGCAGATTAACACAGTTC 516
 Oy 958 TTGACACAGCTCTTAAGTACAGTATGATTAAGATAGCACAGTAAATTTGGAAGTTTCA 1017
 Db 517 TAGGAAGGCTTCAAGAGTGTCTTACAAAGAGTGCACACAAATAGTTGGTGTATGCA 576
 Oy 1018 GAAGTTACAGATCTTGTCTAAGCTTATGCTATGCTATTAATGCAATTGAACAACA 1077
 Db 577 GCACCAAGAGAAATGACTAAGAGGTTGCACAGATCAAAATCTCATGATGAGTACAG 636
 Oy 1078 CTCTACTATTACCGTAAACACTACAAAGCTTTGGGAAATTAAGTGTGTGTAG 1137
 Db 637 AGCAACATCAGAGAGAGAAACTCAATGAATGAAATGCAAAAGTCCCGGTGTGTGTG 696
 Oy 1138 CTGTATCAAGTATGAGCTTCAACAGAGACAGCTTAAAGAAATGAACCT 1190
 Db 697 CTGTATTCAGTGTGGAGCACAACAAAGAACTGATTAAGGAGAAAGATT 749

RESULT 15
 AM310455
 LOCUS 680 bp mRNA EST 31-JAN-2000
 DEFINITION PFOVAFB31J1K Onchocerca volutus adult female cDNA following
 Ivermectin (SAM98PF-OVA) Onchocerca volutus CDNA clone
 PFOVAFB31J 5', mRNA sequence.
 ACCESSION AM310455
 VERSION AM310455.1 GI:6826808
 KEYWORDS EST
 SOURCE Onchocerca volutus.
 ORGANISM Onchocerca volutus.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 Onchocercidae; Onchocerca.
 1 (bases 1 to 680)
 REFERENCE Fischer, P. and Williams, S.A.
 Genes Expressed in adult female stage of Onchocerca volutus
 following treatment with ivermectin
 unpublished (1999)
 JOURNAL COMMENT
 Contact: Peter Fischer
 Molecular Parasitology
 Bernhard Nocht Institute for Tropical Medicine
 Bernhard-Nocht-Strasse 74, 20359 Hamburg, Germany
 Tel.: 49 40 42818 486
 Fax: 49 40 42818 400
 Email: pfischer@bni.uni-hamburg.de
 Seq primer: PBluescript SK.
 FEATURES
 Source Location/Qualifiers
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 /clone_1b="Onchocerca volutus adult female cDNA
 following Ivermectin (SAM98PF-OVA)"
 /sex="female"
 /dev_stage="adult"

/lab_host="XLI-Blue MRF"
 /note="Vector: Lambda Uni-ZAP XR; Site.1: Eco RI; Site.2:
 Xho I; Filarial nematode parasite of humans. Two adult
 female worms of Onchocerca volutus were isolated from
 one consenting patient from western Uganda. The patient
 was treated 28 hours and 7 month before nodulectomy with a
 single dose of 150 mg/kg ivermectin. Adult female worms
 were quick frozen. Their mRNA was converted to
 double-stranded cDNA using reverse transcriptase and
 Oligo(dT) followed by RNase H and DNA pol I. The library
 has 2.9 x 10E5 independent recombinants and the average
 insert size is ~800bp. The library was constructed by
 Peter Fischer with worms provided by Dr. Dietrich W.
 Butler. The library is available from Dr. Steven A.
 Williams (U.S.A.) or Dr. Peter Fischer (Germany), email:
 genome@smith.edu, pfische@bni.com"

BASE COUNT 230 a 93 c 151 g 204 t 2 others
 ORIGIN
 Query Match 13.7%; Score 227.4; DB 114; Length 680;
 Best local Similarity 61.2%; Pred. No. 6.2e-53;
 Matches 385; Conservative 0; Mismatches 241; Indels 3; Gaps 1;

Oy 611 TCAATCATGCTCAGACATGTAATAAGTTCACACCTTGAAACCATTTATCTT 670
 Db 1 TCCGTAATTTTATTAATTAATGAAATGATTTGGAGCTGTGATCATCTCTT 60
 Oy 671 AATCAGGATTAATAAGTTCAAAACATTCACATTTTGCACACTTGAAGAATGCT 730
 Db 61 AATTACAGGAAATAAATTAATTAATTCAGCTTGTCTTCTATTCATGACGTGTGT 120
 Oy 731 TAAACCAACGCTCCATTAATTAATGATGATGATGATGATGATGATGATGATGAT 790
 Db 121 TAAGTGTGTAACCTTTACTATTAATGATGATGATGATGATGATGATGATGATGAT 180
 Oy 791 CTTGTCTTGAACAAGATTCGTGTGCTTCAATGTTGCTGTCAAGCGCAGGAT 850
 Db 181 TTTAGTATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 240
 Oy 851 TGGTATCGTGTAAAGCTATGCTGAAGACATTCATTCCTTGAACAGTGTGTA---CAGT 907
 Db 241 TGGTATTAAGAAAGAAAGATGCTTGAAGTATGATGATGATGATGATGATGATGAT 300
 Oy 908 GATTACAGAGATCTAGAGCTTGAATTAAGATGCTCAATGACAGCCTTGACAGGC 967
 Db 301 CATAAAGATGAATCTGGAGTAAATGGAAGACCTTAACCTTGAAGACCTTGACATTCG 360
 Oy 968 TGCTAAGATTAAGTATTAAGATGACAGTAAATGTTGAAGTTTCAAGAGTTTCA 1027
 Db 361 TAAAAATGTTAAATCACTAAAGATTAATCTCAATTTGTTAGCAAAATGAGATTCTGA 420
 Oy 1028 AGCTATTCGTAACCTTATGCTACTGATTAATCGGAATTAAGAAACAACTTCTACT 1087
 Db 421 CAGAGAAAGAGTGAATTAAGAGATTAATCTCAAAATTAAGCTTCACTTATTA 480
 Oy 1088 TGAACGTGAATAACTACAGAGAGTTTGGCAATTAAGTGTGTGATCTTATCA 1147
 Db 481 TATTAAGAGAAATTAAGAGAGGTTTACCAAAATTAAGAGTGTGTCTTACTATA 540
 Oy 1148 AATGAGAGCTTCAACAGAGAGCTTAAAGAAATTAAGAAATTAAGAAATTAAGAA 1207
 Db 541 AGTTGTGACAGCTCAATTAAGATTAAGAGAGCTTAAAGAGAGCTTAAAGATTAAG 600
 Oy 1208 AATGCTACAGCTGACAGCTTGAAGAG 1236
 Db 601 GCACGCCACAAGAGCTCAATTTAGGAG 629

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